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TECH CENTER



1600

RAW SEQUENCE LISTING

DATE: 06/23/2003

PATENT APPLICATION: US/09/647,140B

TIME: 14:00:58

Input Set : A:\Kruh 140 SequenceListing v2.txt

Output Set: N:\CRF4\06232003\I647140B.raw

3 <110> APPLICANT: Fox Chase Cancer Center
 4 Kruh, Gary D.
 5 Lee, Kun
 6 Belinsky, Martin G.
 7 Bain, Lisa J.
 9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
 10 Nucleic Acids and Methods of Use Thereof
 12 <130> FILE REFERENCE: FCCC 98-02
 14 <140> CURRENT APPLICATION NUMBER: 09/647,140B
 15 <141> CURRENT FILING DATE: 2001-05-21
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
 18 <151> PRIOR FILING DATE: 1999-03-26
 20 <150> PRIOR APPLICATION NUMBER: 60/079,759
 21 <151> PRIOR FILING DATE: 1998-03-27
 23 <150> PRIOR APPLICATION NUMBER: 60/095,153
 24 <151> PRIOR FILING DATE: 1998-08-03
 26 <160> NUMBER OF SEQ ID NOS: 33
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 4231
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|------------|------|
| 37 | ggacaggcgt | ggcggccgga | gccccagcat | ccctgcttga | ggtccaggag | cggagcccgc | 60 |
| 38 | ggccaccgcc | gcctgatcag | cgcgacccc | gcccgcgcc | gccccgccg | gcaagatgct | 120 |
| 39 | gcccgtgtac | caggaggtga | agcccaaccc | gctgcaggac | gcgaacatct | gctcacgcgt | 180 |
| 40 | gttcttcttg | tggctcaatc | ccttgtttaa | aattggccat | aaacggagat | tagaggaaga | 240 |
| 41 | tgatatgtat | tcagtgtctg | cagaagaccg | ctcacagcac | cttgagagag | agttgcaagg | 300 |
| 42 | gttctgggat | aaagaagttt | taagagctga | gaatgacgca | cagaagcctt | ctttaacaag | 360 |
| 43 | agcaatcata | aagtgttact | ggaaatctta | tttagttttg | ggaattttta | cgtaattga | 420 |
| 44 | ggaaagtgcc | aaagtaatcc | agcccatatt | tttgggaaaa | attattaatt | attttgaaaa | 480 |
| 45 | ttatgatccc | atggattctg | tggctttgaa | cacagcgtac | gcctatgcc | cggtgctgac | 540 |
| 46 | tttttgcacg | ctcatttttg | ctatactgca | tcacttatat | ttttatcacg | ttcagtgtgc | 600 |
| 47 | tgggatgagg | ttacgagtag | ccatgtgcc | tatgatttat | cgaaggcac | ttcgtcttag | 660 |
| 48 | taacatggcc | atggggaaga | caaccacagg | ccagatagtc | aatctgctgt | ccaatgatgt | 720 |
| 49 | gaacaagttt | gacaggtga | cagtgttctt | acacttcctg | tgggcaggac | cactgcaggc | 780 |
| 50 | gatcgcatg | actgccctac | tctggatgga | gataggaata | tcgtgccttg | ctgggatggc | 840 |
| 51 | agttctaata | attctcctgc | ccttgcaaa | ctgttttggg | aagttgttct | catcactgag | 900 |
| 52 | gagtaaaact | gcaactttca | cgatgccag | gatcaggacc | atgaatgaag | ttataactgg | 960 |
| 53 | tataaggata | ataaaaatgt | acgcctggga | aaagtcattt | tcaaacttta | ttaccaattt | 1020 |
| 54 | gagaaagaag | gagattttcca | agattctgag | aagttcctgc | ctcaggggga | tgaatttggc | 1080 |
| 55 | ttcgtttttc | agtgcagca | aaatcatcgt | gtttgtgacc | ttcaccacct | acgtgctcct | 1140 |
| 56 | cggcagtggt | atcacagcca | gccgcgtgtt | cgtggcagtg | acgtgtatg | gggctgtgcg | 1200 |

P.6

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| | | | | | | | |
|-----|-------------|-------------|-------------|-------------|-------------|-------------|------|
| 57 | gctgacgggtt | accctcttct | tcccctcagc | cattgagagg | gtgtcagagg | caatcgtcag | 1260 |
| 58 | catccgaaga | atccagacct | ttttgctact | tgatgagata | tcacagcgca | accgtcagct | 1320 |
| 59 | gccgtcagat | ggtaaaaaga | tggtgcatgt | gcaggatttt | actgcttttt | gggataaggc | 1380 |
| 60 | atcagagacc | ccaactctac | aaggcctttc | ctttactgtc | agacctggcg | aattgttagc | 1440 |
| 61 | tgtggtcggc | cccgtgggag | cagggaagtc | atcactgtta | agtgccgtgc | tcggggaatt | 1500 |
| 62 | ggccccaagt | cacgggctgg | tcagcgtgca | tggaagaatt | gcctatgtgt | ctcagcagcc | 1560 |
| 63 | ctgggtgttc | tcgggaactc | tgaggagtaa | tatttttatt | gggaagaaat | atgaaaagga | 1620 |
| 64 | acgatatgaa | aaagtcataa | aggcttgtgc | tctgaaaaag | gatttacagc | tgttggagga | 1680 |
| 65 | tggtgatctg | actgtgatag | gagatcgggg | aaccacgctg | agtggagggc | agaaagcacg | 1740 |
| 66 | ggtaaacctt | gcaagagcag | tgtatcaaga | tgctgacatc | tatctcctgg | acgatcctct | 1800 |
| 67 | cagtgcagta | gatgcggaag | ttagcagaca | cttggttcgaa | ctgtgtattt | gtcaaatttt | 1860 |
| 68 | gcatgagaag | atcacaattt | tagtgactca | tcagttgcag | tacctcaaag | ctgcaagtca | 1920 |
| 69 | gattctgata | ttgaaagatg | gtaaaatggt | gcagaagggg | acttacactg | agttcctaaa | 1980 |
| 70 | atctggtata | gatttttggt | ccctttttaa | gaaggataat | gaggaaagtg | aacaacctcc | 2040 |
| 71 | agttccagga | actcccacac | taaggaatcg | taccttctca | gagtcttcgg | tttgggtctca | 2100 |
| 72 | acaatcttct | agaccctcct | tgaagatggg | tgctctggag | agccaagata | cagagaatgt | 2160 |
| 73 | cccagttaca | ctatcagagg | agaaccgttc | tgaaggaaaa | gttggttttc | aggcctataa | 2220 |
| 74 | gaattacttc | agagctggtg | ctcactggat | tgtcttcatt | ttccttattc | tcctaaacac | 2280 |
| 75 | tgacagctcag | gttgcctatg | tgcttcaaga | ttggtggcct | tcatactggg | caaacaaaca | 2340 |
| 76 | aagtatgcta | aatgtcactg | taaattggagg | aggaaatgta | accgagaagc | tagatcttaa | 2400 |
| 77 | ctggtactta | ggaattttatt | caggtttaac | tgtagctacc | gttctttttg | gcatagcaag | 2460 |
| 78 | atctctattg | gtattctacg | tccttggtta | ctcttcacaa | actttgcaca | acaaaatgtt | 2520 |
| 79 | tgagtcaatt | ctgaaagctc | cggattattt | ctttgataga | aatccaatag | gaagaatttt | 2580 |
| 80 | aaatcgtttc | tccaaagaca | ttggacactt | ggatgatttg | ctgccgctga | cgtttttaga | 2640 |
| 81 | tttcatctcag | acattgctac | aagtggttgg | tgtggtctct | gtggctgtgg | ccgtgattcc | 2700 |
| 82 | ttggatcgca | atacccttgg | ttccccttgg | aatcattttc | atttttcttc | ggcgatattt | 2760 |
| 83 | tttggaacg | tcaagagatg | tgaagcgcct | ggaatctaca | actcggagtc | cagtgttttc | 2820 |
| 84 | ccacttgta | tcttctctcc | aggggctctg | gaccatccgg | gcatacaaag | cagaagagag | 2880 |
| 85 | gtgtcaggaa | ctgtttgatg | cacaccagga | tttacattca | gaggcttggg | tcttgttttt | 2940 |
| 86 | gacaacgtcc | cgctgggttcg | ccgtccgtct | ggatgccatc | tgtgccatgt | ttgtcatcat | 3000 |
| 87 | cgttgccctt | gggtccctga | ttctggcaaa | aactctggat | gccgggcagg | ttggtttggc | 3060 |
| 88 | actgtcctat | gccctcacgc | tcatggggat | gtttcagtg | tgtgttcgac | aaagtgtctga | 3120 |
| 89 | agttgagaat | atgatgatct | cagtagaaa | ggtcattgaa | tacacagacc | ttgaaaaaga | 3180 |
| 90 | agcaccttgg | gaatatcaga | aacgccacc | accagcctgg | ccccatgaag | gagtgataat | 3240 |
| 91 | ctttgacaat | gtgaacttca | tgtacagtcc | aggtgggcct | ctggtactga | agcatctgac | 3300 |
| 92 | agcactcatt | aaatcacaag | aaaaggttgg | cattgtggga | agaaccggag | ctggaaaaag | 3360 |
| 93 | ttccctcatc | tcagcccttt | ttagattgtc | agaaccggaa | ggtaaaattt | ggattgataa | 3420 |
| 94 | gatcttgaca | actgaaattg | gacttcacga | tttaagggaag | aaaatgtcaa | tcatactca | 3480 |
| 95 | ggaacctgtt | ttgttctactg | gaacaatgag | gaaaaacctg | gatcccttta | aggagcacac | 3540 |
| 96 | ggatgaggaa | ctgtggaatg | ccttacaaga | ggtacaactt | aaagaaacca | ttgaagatct | 3600 |
| 97 | tcctggtaaa | atggatactg | aattagcaga | atcaggatcc | aatttttagtg | ttggacaaag | 3660 |
| 98 | acaactggtg | tgccttgcca | gggcaattct | caggaaaaat | cagatattga | ttattgatga | 3720 |
| 99 | agcgacggca | aatgtggatc | caagaactga | tgagttaata | caaaaaaaaa | tccgggagaa | 3780 |
| 100 | atttgcccac | tgcaccgtgc | taaccattgc | acacagattg | aacaccatta | ttgacagcga | 3840 |
| 101 | caagataatg | gttttagatt | cagggaagact | gaaagaatat | gatgagccgt | atgttttgct | 3900 |
| 102 | gcaaaataaa | gagagcctat | tttacaagat | ggtgcaacaa | ctgggcaagg | cagaagccgc | 3960 |
| 103 | tgccctcact | gaaacagcaa | aacagggtata | cttcaaaaga | aattatccac | atattggtca | 4020 |
| 104 | cactgaccac | atggttacaa | acacttccaa | tggacagccc | tcgaccttaa | ctattttcga | 4080 |
| 105 | gacagcactg | tgaatccaac | caaaatgtca | agtcctgttc | gaaggcattt | tccactagtt | 4140 |

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```

106 tttggactat gtaaaccaca ttgtactttt ttttactttg gcaacaaata tttatacata 4200
107 caagatgcta gttcatttga atatttctcc c 4231
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 1325
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
117 1 5 10 15
118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
119 20 25 30
120 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
121 35 40 45
122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
123 50 55 60
124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
125 65 70 75 80
126 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
127 85 90 95
128 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
129 100 105 110
131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
132 115 120 125
133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
134 130 135 140
135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
136 145 150 155 160
137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
138 165 170 175
139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
140 180 185 190
141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
142 195 200 205
143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
144 210 215 220
145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
146 225 230 235 240
147 Met Ala Val Leu Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
148 245 250 255
149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
150 260 265 270
151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
152 275 280 285
153 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
154 290 295 300
155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
156 305 310 315 320
157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
158 325 330 335

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```

159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
160          340          345          350
161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
162          355          360          365
163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164          370          375          380
165 Arg Ile Gln Thr Phe Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166          385          390          395          400
167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168          405          410          415
169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170          420          425          430
171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
172          435          440          445
173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174          450          455          460
175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176          465          470          475          480
177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178          485          490          495
179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180          500          505          510
181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182          515          520          525
183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184          530          535          540
185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186          545          550          555          560
187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188          565          570          575
189 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
190          580          585          590
191 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
192          595          600          605
193 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
194          610          615          620
196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197          625          630          635          640
198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199          645          650          655
200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201          660          665          670
202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203          675          680          685
204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205          690          695          700
206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207          705          710          715          720
208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|
| 209 | | | | 725 | | | | | 730 | | | | 735 | | |
| 210 | Tyr | Trp | Ala | Asn | Lys | Gln | Ser | Met | Leu | Asn | Val | Thr | Val | Asn | Gly |
| 211 | | | | 740 | | | | | 745 | | | | 750 | | |
| 212 | Gly | Asn | Val | Thr | Glu | Lys | Leu | Asp | Leu | Asn | Trp | Tyr | Leu | Gly | Ile |
| 213 | | | | 755 | | | | 760 | | | | | 765 | | |
| 214 | Ser | Gly | Leu | Thr | Val | Ala | Thr | Val | Leu | Phe | Gly | Ile | Ala | Arg | Ser |
| 215 | | | | 770 | | | | 775 | | | | | 780 | | |
| 216 | Leu | Val | Phe | Tyr | Val | Leu | Val | Asn | Ser | Ser | Gln | Thr | Leu | His | Asn |
| 217 | | | | | | | | 790 | | | | | 795 | | |
| 218 | Met | Phe | Glu | Ser | Ile | Leu | Lys | Ala | Pro | Val | Leu | Phe | Phe | Asp | Arg |
| 219 | | | | | | | | 805 | | | | | 810 | | |
| 220 | Pro | Ile | Gly | Arg | Ile | Leu | Asn | Arg | Phe | Ser | Lys | Asp | Ile | Gly | His |
| 221 | | | | | | | | 820 | | | | | 825 | | |
| 222 | Asp | Asp | Leu | Leu | Pro | Leu | Thr | Phe | Leu | Asp | Phe | Ile | Gln | Thr | Leu |
| 223 | | | | | | | | 835 | | | | | 840 | | |
| 224 | Gln | Val | Val | Gly | Val | Val | Ser | Val | Ala | Val | Ala | Val | Ile | Pro | Trp |
| 225 | | | | | | | | 845 | | | | | 850 | | |
| 226 | Ala | Ile | Pro | Leu | Val | Pro | Leu | Gly | Ile | Ile | Phe | Ile | Phe | Leu | Arg |
| 227 | | | | | | | | 855 | | | | | 860 | | |
| 228 | Tyr | Phe | Leu | Glu | Thr | Ser | Arg | Asp | Val | Lys | Arg | Leu | Glu | Ser | Thr |
| 229 | | | | | | | | 865 | | | | | 870 | | |
| 230 | Arg | Ser | Pro | Val | Phe | Ser | His | Leu | Ser | Ser | Ser | Leu | Gln | Gly | Leu |
| 231 | | | | | | | | 885 | | | | | 890 | | |
| 232 | Thr | Ile | Arg | Ala | Tyr | Lys | Ala | Glu | Glu | Arg | Cys | Gln | Glu | Leu | Phe |
| 233 | | | | | | | | 895 | | | | | 900 | | |
| 234 | Ala | His | Gln | Asp | Leu | His | Ser | Glu | Ala | Trp | Phe | Leu | Phe | Leu | Thr |
| 235 | | | | | | | | 905 | | | | | 910 | | |
| 236 | Ser | Arg | Trp | Phe | Ala | Val | Arg | Leu | Asp | Ala | Ile | Cys | Ala | Met | Phe |
| 237 | | | | | | | | 915 | | | | | 920 | | |
| 238 | Ile | Ile | Val | Ala | Phe | Gly | Ser | Leu | Ile | Leu | Ala | Lys | Thr | Leu | Asp |
| 239 | | | | | | | | 925 | | | | | 930 | | |
| 240 | Gly | Gln | Val | Gly | Leu | Ala | Leu | Ser | Tyr | Ala | Leu | Thr | Leu | Met | Gly |
| 241 | | | | | | | | 935 | | | | | 940 | | |
| 242 | Phe | Gln | Trp | Cys | Val | Arg | Gln | Ser | Ala | Glu | Val | Glu | Asn | Met | Met |
| 243 | | | | | | | | 945 | | | | | 950 | | |
| 244 | Ser | Val | Glu | Arg | Val | Ile | Glu | Tyr | Thr | Asp | Leu | Glu | Lys | Glu | Ala |
| 245 | | | | | | | | 955 | | | | | 960 | | |
| 246 | Trp | Glu | Tyr | Gln | Lys | Arg | Pro | Pro | Pro | Ala | Trp | Pro | His | Glu | Gly |
| 247 | | | | | | | | 965 | | | | | 970 | | |
| 248 | Ile | Ile | Phe | Asp | Asn | Val | Asn | Phe | Met | Tyr | Ser | Pro | Gly | Gly | Pro |
| 249 | | | | | | | | 975 | | | | | 980 | | |
| 250 | Val | Leu | Lys | His | Leu | Thr | Ala | Leu | Ile | Lys | Ser | Gln | Glu | Lys | Val |
| 251 | | | | | | | | 985 | | | | | 990 | | |
| 252 | Ile | Val | Gly | Arg | Thr | Gly | Ala | Gly | Lys | Ser | Ser | Leu | Ile | Ser | Ala |
| 253 | | | | | | | | 995 | | | | | 1000 | | |
| 254 | Phe | Arg | Leu | Ser | Glu | Pro | Glu | Gly | Lys | Ile | Trp | Ile | Asp | Lys | Ile |
| 255 | | | | | | | | 1005 | | | | | 1010 | | |
| 256 | Thr | Thr | Glu | Ile | Gly | Leu | His | Asp | Leu | Arg | Lys | Lys | Met | Ser | Ile |
| 257 | | | | | | | | 1015 | | | | | 1020 | | |

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 18
Seq#:16; N Pos. 4,7,10,13,16,19
Seq#:17; N Pos. 23,29
Seq#:18; N Pos. 9,18